

RAW SEQUENCE LISTING

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Application Serial Number: 10/516,342
Source: PCT
Date Processed by STIC: 01/10/2006

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DATE: 01/10/2006

PATENT APPLICATION: US/10/516,342

TIME: 08:40:50

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J516342.raw

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5 <110> APPLICANT: Memorial Sloan-Kettering Cancer Center
7      Kolesnick, Richard N.
9      Xing, Hong-Mei R.
13 <120> TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS
MEDIATED
14      TUMORIGENESIS
18 <130> FILE REFERENCE: 1216-1-006PCT
W--> 19 US
22 <140> CURRENT APPLICATION NUMBER: 10/516,342
23 <141> CURRENT FILING DATE: 2004-11-30
25 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
26 <151> PRIOR FILING DATE: 2003-05-29
29 <150> PRIOR APPLICATION NUMBER: 60/384,228
31 <151> PRIOR FILING DATE: 2002-05-30
35 <150> PRIOR APPLICATION NUMBER: 60/460,023
37 <151> PRIOR FILING DATE: 2003-04-03
41 <160> NUMBER OF SEQ ID NOS: 23
45 <170> SOFTWARE: PatentIn version 3.1
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 120
53 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
59 <400> SEQUENCE: 1
60 ctgcagaagc tcatcgatat ctccatcggc agtctgcgcg ggctgcgcac caagtgctca      60
62 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac      120
65 <210> SEQ ID NO: 2
67 <211> LENGTH: 41
69 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2
77 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
78 1          5          10          15
81 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
82          20          25          30
85 Leu Glu Ala Lys Leu Val Lys Tyr Ile
86          35          40
89 <210> SEQ ID NO: 3
91 <211> LENGTH: 19
93 <212> TYPE: DNA
95 <213> ORGANISM: Homo sapiens
99 <400> SEQUENCE: 3
100 ggcagtcctgc gcgggctgc
103 <210> SEQ ID NO: 4
105 <211> LENGTH: 18

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107 <212> TYPE: DNA
109 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 4
114 tcagtgtcta acgacctc 18
117 <210> SEQ ID NO: 5
119 <211> LENGTH: 18
121 <212> TYPE: DNA
123 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 5
128 cggaccctag aggcaaag 18
131 <210> SEQ ID NO: 6
133 <211> LENGTH: 19
135 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
143 <223> OTHER INFORMATION: antisense oligonucleotide
145 <400> SEQUENCE: 6
146 cagcccgccg agactgccg 19
149 <210> SEQ ID NO: 7
151 <211> LENGTH: 18
153 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
161 <223> OTHER INFORMATION: antisense oligonucleotide
163 <400> SEQUENCE: 7
164 gaggtcggtta gacactga 18
167 <210> SEQ ID NO: 8
169 <211> LENGTH: 16
171 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: antisense oligonucleotide
181 <400> SEQUENCE: 8
182 ctttgcctct aggggtc 16
185 <210> SEQ ID NO: 9
187 <211> LENGTH: 873
189 <212> TYPE: PRT
191 <213> ORGANISM: Mus musculus
195 <400> SEQUENCE: 9
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198 1 5 10 15
201 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
202 20 25 30
205 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
206 35 40 45
209 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
210 50 55 60
213 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
214 65 70 75 80

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217 Tyr Ile Cys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp
218                               85                               90                               95
221 Arg Thr Ala Glu Leu Asn Ser Tyr Pro Arg Phe Ser Asp Trp Leu Tyr
222                               100                              105                              110
225 Ile Phe Asn Val Arg Pro Glu Val Val Gln Glu Ile Pro Gln Glu Leu
226                               115                              120                              125
229 Thr Leu Asp Ala Leu Leu Glu Met Asp Glu Ala Lys Ala Lys Glu Met
230                               130                              135                              140
233 Leu Arg Arg Trp Gly Ala Ser Thr Glu Glu Cys Ser Arg Leu Gln Gln
234 145                               150                              155                              160
237 Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly Gly Glu His Lys
238                               165                              170                              175
241 Met Asp Ser Gly Trp Ser Ser Thr Asp Ala Arg Asp Ser Ser Leu Gly
242                               180                              185                              190
245 Pro Pro Met Asp Met Leu Ser Ser Ser Leu Gly Arg Ala Gly Ala Ser Thr
246                               195                              200                              205
249 Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser
250                               210                              215                              220
253 Pro Val Pro Gly Leu Ser Glu Gly Leu Ser Asp Ser Cys Ile Pro Leu
254 225                               230                              235                              240
257 His Thr Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser Phe Ile Thr
258                               245                              250                              255
261 Pro Pro Thr Thr Pro Gln Leu Arg Arg His Ala Lys Leu Lys Pro Pro
262                               260                              265                              270
265 Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu Leu Pro Ser
266                               275                              280                              285
269 Phe Pro Thr Leu Thr Arg Ser Lys Ser His Glu Ser Gln Leu Gly Asn
270                               290                              295                              300
273 Arg Ile Asp Asp Val Thr Pro Met Lys Phe Glu Leu Pro His Gly Ser
274 305                               310                              315                              320
277 Pro Gln Leu Val Arg Arg Asp Ile Gly Leu Ser Val Thr His Arg Phe
278                               325                              330                              335
281 Ser Thr Lys Ser Trp Leu Ser Gln Val Cys Asn Val Cys Gln Lys Ser
282                               340                              345                              350
285 Met Ile Phe Gly Val Lys Cys Lys His Cys Arg Leu Lys Cys His Asn
286                               355                              360                              365
289 Lys Cys Thr Lys Glu Ala Pro Ala Cys Arg Ile Thr Phe Leu Pro Leu
290                               370                              375                              380
293 Ala Arg Leu Arg Arg Thr Glu Ser Val Pro Ser Asp Ile Asn Asn Pro
294 385                               390                              395                              400
297 Val Asp Arg Ala Ala Glu Pro His Phe Gly Thr Leu Pro Lys Ala Leu
298                               405                              410                              415
301 Thr Lys Lys Glu His Pro Pro Ala Met Asn Leu Asp Ser Ser Ser Asn
302                               420                              425                              430
305 Pro Ser Ser Thr Thr Ser Ser Thr Pro Ser Ser Pro Ala Pro Phe Leu
306                               435                              440                              445
309 Thr Ser Ser Asn Pro Ser Ser Ala Thr Thr Pro Pro Asn Pro Ser Pro
310                               450                              455                              460
313 Gly Gln Arg Asp Ser Arg Phe Ser Phe Pro Asp Ile Ser Ala Cys Ser

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314 465          470          475          480
317 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp
318          485          490          495
321 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
322          500          505          510
325 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
326          515          520          525
329 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
330          530          535          540
333 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
334 545          550          555          560
337 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
338          565          570          575
341 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
342          580          585          590
345 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
346          595          600          605
349 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
350          610          615          620
353 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
354 625          630          635          640
357 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
358          645          650          655
361 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
362          660          665          670
365 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
366          675          680          685
369 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
370          690          695          700
373 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
374 705          710          715          720
377 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
378          725          730          735
381 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
382          740          745          750
385 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
386          755          760          765
389 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
390          770          775          780
393 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
394 785          790          795          800
397 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
398          805          810          815
401 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
402          820          825          830
405 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
406          835          840          845
409 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
410          850          855          860

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413 Thr Leu Glu Ser Gly Asn Pro Lys Met
414 865                               870
417 <210> SEQ ID NO: 10
419 <211> LENGTH: 866
421 <212> TYPE: PRT
423 <213> ORGANISM: Homo sapiens
427 <400> SEQUENCE: 10
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430 1                               5                               10                               15
433 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
434                               20                               25                               30
437 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
438                               35                               40                               45
441 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
442                               50                               55                               60
445 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
446 65                               70                               75                               80
449 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
450                               85                               90                               95
453 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
454                               100                              105                              110
457 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
458                               115                              120                              125
461 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
462                               130                              135                              140
465 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
466 145                              150                              155                              160
469 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
470                               165                              170                              175
473 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
474                               180                              185                              190
477 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
478                               195                              200                              205
481 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
482                               210                              215                              220
485 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
486 225                              230                              235                              240
489 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
490                               245                              250                              255
493 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
494                               260                              265                              270
497 Lys Pro Pro Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
498                               275                              280                              285
501 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
502                               290                              295                              300
505 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
506 305                              310                              315                              320
509 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
510                               325                              330                              335

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VERIFICATION SUMMARY

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